

OIEP

# 9

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/824,551

DATE: 12/14/2001

TIME: 12:37:45

Input Set : A:\Ma280106.app

Output Set: N:\CRF3\12142001\I824551.raw

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3 <110> APPLICANT: BATHE, BRIGITTE
4   KREUTZER, CAROLINE
5   MARX, ACHIM
6   PFEFFERLE, WALTER
8 <120> TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE
9   LUXS GENE
11 <130> FILE REFERENCE: MAS/21123/280106
13 <140> CURRENT APPLICATION NUMBER: 09/824,551
14 <141> CURRENT FILING DATE: 2001-04-04
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1902
22 <212> TYPE: DNA
23 <213> ORGANISM: Corynebacterium glutamicum
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (342)..(1610)
28 <223> OTHER INFORMATION: luxS-Gen
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31 ggtaggagta aaaaacgcag gagggcgctcg aaaagcgctc gtctgtgccg taaccocgtga 60
33 cgcgctggcc gttggtatcg gcgaccagc cgggtgccag gtaggggcat gcggtttgtg 120
35 cgggtgcgttc gaccgcgggc atcgcgctcg tgggaaggcc gtcagtaatt acttccgggg 180
37 ctgcctcggt ggtggtctct ggggttgcct caggttccgc cggggtacaa gcggtgagca 240
39 tgatggaagc agcgaggata gtaggtaatg tacgacgcag gcagtcaagc ctagatcgtg 300
41 tgtcggaaac cggacgcaat gagctcgatg ttgaaaccct t gtg aag aag ggg aat 356
42                                     Met Lys Lys Gly Asn
43                                     1      5
45 caa ccg ggc gcg atg agc tat cgc aac agt atc cac att ttg aca gcc 404
46 Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile His Ile Leu Thr Ala
47      10      15      20
49 tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc cgc ctg acg ctg ccg 452
50 Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro
51      25      30      35
53 atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg tgg ggt ttt ctg tac 500
54 Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val Trp Gly Phe Leu Tyr
55      40      45      50
57 ttc tat gga tca acc aaa cgc gta gat ttg agc cac ggc atg cag ctg 548
58 Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser His Gly Met Gln Leu
59      55      60      65
61 ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att ttt atg gtg ccg atc 596
62 Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile Phe Met Val Pro Ile
63 70      75      80      85
65 gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg ttt ttc ctc tat cta 644
66 Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu
67      90      95      100
69 cag gtg atg cct gac gtg aga ggc att att gcg att ttg ggt gcg aca 692

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70 Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr
71          105          110          115
73 gcg att gcg att gcc agc cag tat tcc gtg ggg ttg acc ttt ggt ggt 740
74 Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly
75          120          125          130
77 gtg atg ggt ccg gtg gtc tct gcg atc gtg acc gtg gct att gat tac 788
78 Val Met Gly Pro Val Val Ser Ala Ile Val Thr Val Ala Ile Asp Tyr
79          135          140          145
81 gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa aag cag gaa ttg att 836
82 Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu Lys Gln Glu Leu Ile
83 150          155          160          165
85 gat cag ttg att gaa act cgc tcc cag ctg gcg gtg acg gaa cga aat 884
86 Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala Val Thr Glu Arg Asn
87          170          175          180
89 gcg ggt att gct gcg gaa cgt caa cgt att gcg cat gaa att cat gac 932
90 Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala His Glu Ile His Asp
91          185          190          195
93 acg gtc gcc cag gga ctc tcc tcc att caa atg ctg ctg cat gtc tct 980
94 Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met Leu Leu His Val Ser
95          200          205          210
97 gaa cag gag att ctc gtt gct gag atg gaa gag aag cca aag gag gcg 1028
98 Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu Lys Pro Lys Glu Ala
99          215          220          225
101 atc gtg aag aag atg cgc ctt gcc cga caa aca gcc tcc gac aat ctc 1076
102 Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu
103 230          235          240          245
105 agt gag gct cgc gcg atg att gcg gcg ttg caa ccg gca gcg ctg tct 1124
106 Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser
107          250          255          260
109 aaa acc tcc ttg gaa gca gca ctt cac cgc gtc aca gaa ccg ttg ttg 1172
110 Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val Thr Glu Pro Leu Leu
111          265          270          275
113 ggt att aat ttt gtg att tct gtc gac ggt gat gtt cgc caa ctg ccc 1220
114 Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp Val Arg Gln Leu Pro
115          280          285          290
117 atg aaa act gaa gcc acc ctt ctg cga att gct caa ggt gcg atc gga 1268
118 Met Lys Thr Glu Ala Thr Leu Arg Ile Ala Gln Gly Ala Ile Gly
119          295          300          305
121 aat gtg gcg aaa cat tca gag gcg aaa aac tgc cac gtg aca cta acc 1316
122 Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys His Val Thr Leu Thr
123 310          315          320          325
125 tac gaa gac aca gaa gta cgc ctt gat gtg gtt gat gac ggt gtg ggt 1364
126 Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val Asp Asp Gly Val Gly
127          330          335          340
129 ttt gag cct tcg gaa gtg tcc agt acc ccc gct ggc ctt ggc cat atc 1412
130 Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala Gly Leu Gly His Ile
131          345          350          355
133 ggc tta acc gca ttg cag cag cgt gcg atg gaa ttg cac ggc gaa gtt 1460
134 Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu Leu His Gly Glu Val

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135          360          365          370
137 ata gtg gaa tct gca tat ggg cag ggt act gcg gta tct gca gca ttg 1508
138 ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala Val Ser Ala Ala Leu
139          375          380          385
141 ccg gtg gag cca cca gag ggg ttt gtc ggg gcg ccg gtt ttg gca gat 1556
142 Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala Pro Val Leu Ala Asp
143 390          395          400          405
145 tcg gac tca agt gct aca ggc gag gtt gaa cta agt tct cca act gac 1604
146 Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu Ser Ser Pro Thr Asp
147          410          415          420
149 gat gag taaggctaga ctaaagtacg attcatctgc tcatcgatac tcttgaaggc 1660
150 Asp Glu
152 gcattttcat tcgaaacgaa gtgcgccatt gggaaggacc tagttcaaac aatgattcgc 1720
154 gtgctgcttg ctgatgacca cgaaatcggt aggtctggac tccgagctgt gctggaaagc 1780
156 gccgaggaca ttgaagtgtt gggcgaagtc tccaccgcg aaggtgcggt gcaggcagcc 1840
158 caagaaggcg gaatcgacgt catcttgatg gacctccgat tcggccccgg cgtccaagga 1900
160 ac 1902
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 423
165 <212> TYPE: PRT
166 <213> ORGANISM: Corynebacterium glutamicum
168 <400> SEQUENCE: 2
169 Met Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
170 1 5 10 15
172 His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala
173 20 25 30
175 Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
176 35 40 45
178 Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
179 50 55 60
181 His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
182 65 70 75 80
184 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
185 85 90 95
187 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
188 100 105 110
190 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
191 115 120 125
193 Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
194 130 135 140
196 Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
197 145 150 155 160
199 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
200 165 170 175
202 Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
203 180 185 190
205 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
206 195 200 205
208 Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu

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209      210      215      220
211 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
212 225      230      235      240
214 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln
215      245      250      255
217 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
218      260      265      270
220 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
221      275      280      285
223 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
224      290      295      300
226 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
227 305      310      315      320
229 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
230      325      330      335
232 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
233      340      345      350
235 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
236      355      360      365
238 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
239      370      375      380
241 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
242 385      390      395      400
244 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
245      405      410      415
247 Ser Ser Pro Thr Asp Asp Glu
248      420
252 <210> SEQ ID NO: 3
253 <211> LENGTH: 20
254 <212> TYPE: DNA
255 <213> ORGANISM: Corynebacterium glutamicum
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Primer luxS-int1
260 <400> SEQUENCE: 3
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264 <210> SEQ ID NO: 4
265 <211> LENGTH: 20
266 <212> TYPE: DNA
267 <213> ORGANISM: Corynebacterium glutamicum
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Primer luxS-int2
272 <400> SEQUENCE: 4
273 ottgagcaat tcgcagaagg

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VERIFICATION SUMMARY

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